

Application No.: 10/517,741  
Attorney Docket No.: 47675-93  
First Applicant's Name: John Foekens  
Application Filing Date: 03 January 2006  
Office Action Dated: 24 November 2008  
Date of Response: 26 May 2009  
Examiner: Carla J. Myers

IN THE SPECIFICATION:

Applicants, pursuant to 37 C.F.R. § 1.121, submit the following amendments to the Specification:

Kindly **add** the following title to page 32 prior to the final paragraph:

--Brief Description of the Drawings--

Kindly **substitute** the following paragraph for the corresponding paragraph on pages 34-35 of the original filed application:

--Figures 5 to 12 show a ranked matrix of additional data obtained according to Example 1 (Dataset 1) according to CpG methylation differences between the two classes of tissues, using an algorithm. Figures 5, 7, 9 and 11 are shown in greyscale, wherein the most significant CpG positions are at the bottom of the matrix with significance decreasing towards the top. Black indicates total methylation at a given CpG position, white represents no methylation at the particular position, with degrees of methylation represented in grey, from light (low proportion of methylation) to dark (high proportion of methylation). Each row represents one specific CpG position within a gene and each column shows the methylation profile for the different CpGs for one sample. On the left side the gene name is shown, on the right side p values for the individual CpG positions are shown. The p values are the probabilities that the observed distribution occurred by chance in the data set. Figures 6, 8, 10 and 12 are true black and white copies of the original red-green versions of the preceding figures (i.e. figures 5, 7, 9 and 11 respectively). ~~Red indicates total methylation at a given CpG position, green represents no methylation at the particular position.~~--

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Kindly *substitute* the following paragraph for the corresponding paragraph on page 35 of the original filed application:

--Figure 19 shows the Kaplan-Meier estimated disease-free survival curves for the gene PITX2, the dotted line (upper curve) shows responders~~non-responders~~ whereas the unbroken line (lower curve) shows non-responders~~responders~~.--